

BLASTP 2.2.10 [Oct-19-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1109960786-8874-77563893168.BLASTQ2

Query=

(60 letters)

Database: All non-redundant GenBank CDS

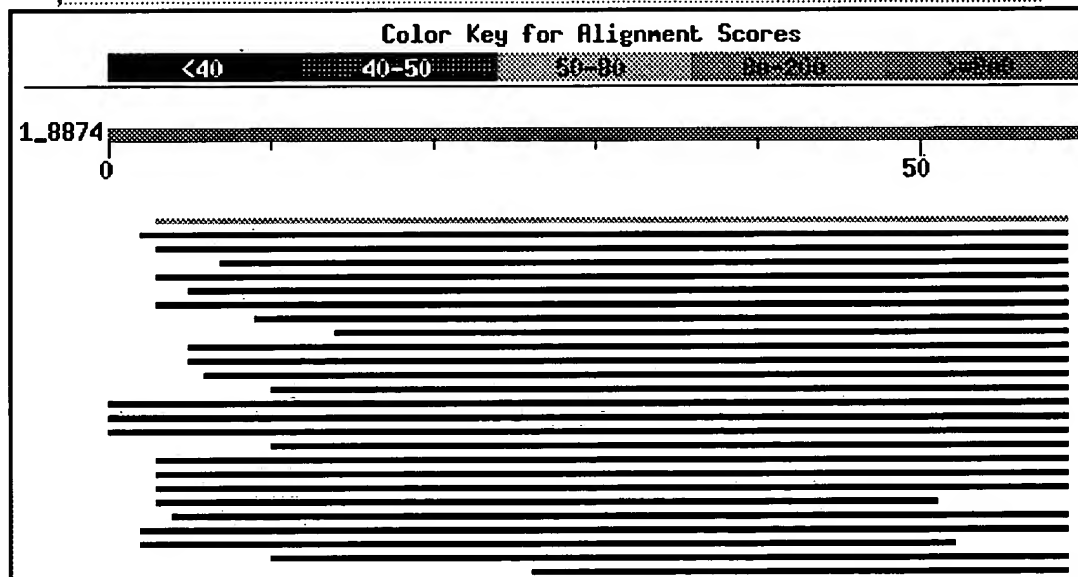
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
2,340,000 sequences; 793,074,205 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 26 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi 46580775 ref YP_011583.1 	outer membrane protein OmpH, p...	55	7e-07	
gi 54030341 ref ZP_00362479.1 	COG2825: Outer membrane prot...	39	0.030	
gi 28851988 gb AAO55063.1 	outer membrane protein OmpH, put...	39	0.039	
gi 48732730 ref ZP_00266473.1 	COG2825: Outer membrane prot...	39	0.052	
gi 48768198 ref ZP_00272549.1 	COG2825: Outer membrane prot...	38	0.088	
gi 47575422 ref ZP_00245457.1 	COG2825: Outer membrane prot...	38	0.088	
gi 26988332 ref NP_743757.1 	outer membrane protein OmpH [P...	37	0.15	

gi 46188414 ref ZP_00125848.2 	COG2825: Outer membrane prot...	37	0.20	
gi 41725330 ref ZP_00152088.1 	COG2825: Outer membrane prot...	36	0.33	
gi 33596183 ref NP_883826.1 	putative outer membrane protei...	35	0.57	G
gi 33592526 ref NP_880170.1 	putative outer membrane protei...	35	0.57	G
gi 17428428 emb CAD15115.1 	PROBABLE TRANSMEMBRANE PROTEIN ...	35	0.57	G
gi 48787685 ref ZP_00283664.1 	COG2825: Outer membrane prot...	34	1.3	
gi 52006428 ref ZP_00333808.1 	COG2825: Outer membrane prot...	33	1.7	
gi 53719759 ref YP_108745.1 	putative outer membrane protei...	33	2.8	G
gi 9949807 qb AAG07035.1 	probable outer membrane protein p...	33	2.8	G
gi 49081394 qb AAT50125.1 	PA3647 [synthetic construct]	33	2.8	
gi 51597309 ref YP_071500.1 	cationic 19 kDa outer membrane...	32	4.8	G
gi 45442565 ref NP_994104.1 	cationic 19 kDa outer membrane...	32	4.8	G
gi 16121353 ref NP_404666.1 	cationic 19 kDa outer membrane...	32	4.8	G
gi 51246715 ref YP_066599.1 	hypothetical protein DP2863 [D...	32	4.8	G
gi 46164357 ref ZP_00205054.1 	COG2825: Outer membrane prot...	32	4.8	
gi 30249671 ref NP_841741.1 	putative transmembrane protein...	32	6.3	G
gi 34103516 qb AAQ59878.1 	outer membrane protein [Chromoba...	32	6.3	G
gi 46319050 ref ZP_00219470.1 	COG2825: Outer membrane prot...	32	6.3	
gi 53761352 ref ZP_00166830.2 	COG2825: Outer membrane prot...	31	8.2	

Alignments

Get selected sequences

Select all

Deselect all

☒ >[gi|46580775|ref|YP_011583.1|](#) **G** outer membrane protein OmpH, putative [Desulfovibrio subsp. vulgaris str. Hildenborough]
[gi|46450195|qb|AAS96843.1|](#) **G** outer membrane protein OmpH, putative [Desulfovibrio subsp. vulgaris str. Hildenborough]
Length = 175

Score = 54.7 bits (130), Expect = 7e-07
Identities = 26/57 (45%), Positives = 39/57 (68%)

Query: 4 KTLMAILACLLVANSFAFSADFPVGFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
K L A+ A L+ A++A +AD +G+ N Q +A + EAA+ AQKK+++ FG EK QL
Sbjct: 3 KILVFAVAFLMAASTAMAADLKVGVNMQKLATQCEAAQEAQKKMKATFGPEKDQL 59

☒ >[gi|54030341|ref|ZP_00362479.1|](#) COG2825: Outer membrane protein [Polaromonas sp.]
Length = 168

Score = 39.3 bits (90), Expect = 0.030
Identities = 23/61 (37%), Positives = 34/61 (55%), Gaps = 3/61 (4%)

Query: 3 VKTLMAILACLLVANSFAFSA---DFPIGVGFNSQSIAMESEAAKAAQKKLQSEFGNEKTQ 59
+K S I ++A + FSA +F +GV N I E+ +AKAAQ KL+ EF + +
Sbjct: 1 MKHFSTKIFLGCVIALAGFSASAQEFKGVVNLDRIFREANSAAQTKLEQEFKREKE 60

Query: 60 L 60

L

Sbjct: 61 L 61

☒ >[gi|28851988|qb|AAO55063.1|](#) **G** outer membrane protein OmpH, putative [Pseudomonas tomato str. DC3000]

[gi|28868749|ref|NP_791368.1|](#) **G** outer membrane protein OmpH, putative [Pseudomonas tomato str. DC3000]

Length = 167

Score = 38.9 bits (89), Expect = 0.039

Identities = 23/57 (40%), Positives = 33/57 (57%), Gaps = 1/57 (1%)

Query: 4 KTLMAILACLLVANSAFSADFPVFNFSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
K + +LA +LVA+ AF AD I V N Q +ES+AAK + +FG + T+L
Sbjct: 3 KLTQLVLLATVVLVAF-ADMKIAVLNYQMALLESDAAKKYAVDAEKKFGPQLTKL 58

>[gi|48732730|ref|ZP_00266473.1|](#) COG2825: Outer membrane protein [Pseudomonas fl
Length = 161

Score = 38.5 bits (88), Expect = 0.052

Identities = 23/53 (43%), Positives = 31/53 (58%), Gaps = 1/53 (1%)

Query: 8 MAILACLLVANSAFSADFPVFNFSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
M +LA +LVA AF AD I V N Q +ES+AAK + +FG + T+L
Sbjct: 1 MVLLASVLVAGPAF-ADMKIAVLNYQMALLESDAAKKYAVDAEKKFGPQLTKL 52

>[gi|48768198|ref|ZP_00272549.1|](#) COG2825: Outer membrane protein [Ralstonia meta
Length = 177

Score = 37.7 bits (86), Expect = 0.088

Identities = 24/59 (40%), Positives = 32/59 (54%), Gaps = 2/59 (3%)

Query: 4 KTLMAILAC--LLVANSAFSADFPVFNFSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
K+LS A LA L A A + + I NS+ I +S+ AKAAQ KL+ EF +L
Sbjct: 9 KSLSAALAAAAALCAAAPAMAQEARIAAVNSERILRDSQPAKAAQVKLEQEFKRDREL 67

>[gi|47575422|ref|ZP_00245457.1|](#) COG2825: Outer membrane protein [Rubrivivax gela
Length = 163

Score = 37.7 bits (86), Expect = 0.088

Identities = 22/55 (40%), Positives = 33/55 (60%), Gaps = 2/55 (3%)

Query: 6 LSMAILACLLVANSAFSADFPVFNFSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
L+ A+LA + A +A + IG NS+ + E+ AKAAQ KL+SEF + +L
Sbjct: 4 LAAAVLAAGVTAAAA--QELKIGYVNSERVLREAGPAKAAQAKLESEFSKREKEL 56

>[gi|26988332|ref|NP_743757.1|](#) **G** outer membrane protein OmpH [Pseudomonas putida
[gi|24983081|gb|AAN67221.1|](#) **G** outer membrane protein OmpH [Pseudomonas putida KT24
Length = 167

Score = 37.0 bits (84), Expect = 0.15

Identities = 21/57 (36%), Positives = 32/57 (56%), Gaps = 1/57 (1%)

Query: 4 KTLMAILACLLVANSAFSADFPVFNFSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
K +A++A LVA AF A+ + V N Q +ES+AAK + +FG + T+L
Sbjct: 3 KLAQLAVVAAALVATPAF-AEMKVAVLNYQMALLESDAAKKYAVDAEKKFGPQLTKL 58

>[gi|46188414|ref|ZP_00125848.2|](#) COG2825: Outer membrane protein [Pseudomonas sy
syringae B728a]
Length = 159

Score = 36.6 bits (83), Expect = 0.20



Identities = 22/51 (43%), Positives = 31/51 (60%), Gaps = 1/51 (1%)

Query: 10 ILACLLVANSAFSADFPVIGVNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
+LA +LVA+ AF AD I V N Q +ES+AAK + +FG + T+L
Sbjct: 1 MLATVLVASPAF-ADMKIAVLNYQMALLESDAAKRYAVDAEKKFGPQLTKL 50

>[gi|41725330|ref|ZP_00152088.1|](#) COG2825: Outer membrane protein [Dechloromonas] :
Length = 156





Score = 35.8 bits (81), Expect = 0.33
Identities = 17/46 (36%), Positives = 26/46 (56%)

Query: 15 LVANSAFSADFPVIGVNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
L A A++A+ +G N+Q I ++ AA+ A KKL+ EF L
Sbjct: 4 LFATGAYAAELKVG YVNTQRIFRDAPAAQKAACKLEGEFAKRDQDL 49

>[gi|33596183|ref|NP_883826.1|](#)  putative outer membrane protein [Bordetella par] :
[gi|33573186|emb|CAE36838.1|](#)  putative outer membrane protein [Bordetella paraper] :
Length = 203



Score = 35.0 bits (79), Expect = 0.57
Identities = 22/59 (37%), Positives = 32/59 (54%), Gaps = 4/59 (6%)

Query: 6 LSMAILACLLVANSAF----SADFPVIGVNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
+S+A+ LL +SA + IG N++ I ES AKAAQ K++SEF +L
Sbjct: 40 VSLALAGALLFGSSAAVTAQAQGTKIGFVNTERILRESGPAKAAQSKIESEFKRRDDEL 98

>[gi|33592526|ref|NP_880170.1|](#)  putative outer membrane protein [Bordetella pert] :
[gi|33601591|ref|NP_889151.1|](#)  putative outer membrane protein [Bordetella bronch] :
[gi|33576027|emb|CAE33107.1|](#)  putative outer membrane protein [Bordetella bronchi] :
[gi|33572172|emb|CAE41718.1|](#)  putative outer membrane protein [Bordetella pertuss] :
Length = 187

Score = 35.0 bits (79), Expect = 0.57
Identities = 22/59 (37%), Positives = 32/59 (54%), Gaps = 4/59 (6%)

Query: 6 LSMAILACLLVANSAF----SADFPVIGVNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
+S+A+ LL +SA + IG N++ I ES AKAAQ K++SEF +L
Sbjct: 24 VSLALAGALLFGSSAAVTAQAQGTKIGFVNTERILRESGPAKAAQSKIESEFKRRDDEL 82

>[gi|17428428|emb|CAD15115.1|](#)  PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanac] :
[gi|17546132|ref|NP_519534.1|](#)  PROBABLE TRANSMEMBRANE PROTEIN [Ralstonia solanace] :
Length = 184

Score = 35.0 bits (79), Expect = 0.57
Identities = 20/54 (37%), Positives = 29/54 (53%)

Query: 7 SMAILACLLVANSAFSADFPVIGVNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
+ A LA A A + + I NS+ I +S+ AKAAQ KL++EF +L
Sbjct: 21 AFAALAAASFALPATAQEARIAAVNSERILRDSQPAKAAQAKLETEFAKRDREL 74

>[gi|48787685|ref|ZP_00283664.1|](#) COG2825: Outer membrane protein [Burkholderia fu] :
Length = 169





Score = 33.9 bits (76), Expect = 1.3
Identities = 21/50 (42%), Positives = 24/50 (48%)

Query: 11 LACLLVANSAFSADFP-IGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
LA L A + I NS I ES AAKAAQ KL++EF L
Sbjct: 12 LAMTLGVGVAHGQEARIAAVNSDRILRESAAKAAQVKLEAEFAKRDKDL 61

>[gi|52006428|ref|ZP_00333808.1|](#) COG2825: Outer membrane protein [Thiobacillus de
25259]
Length = 167



Score = 33.5 bits (75), Expect = 1.7
Identities = 17/60 (28%), Positives = 29/60 (48%)

Query: 1 MKVKTLMAILACLLVANSAFSADFP-IGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
M K +++++ AD IG N++ + E+ + AAQKKL+ EF +L
Sbjct: 2 MSFKQFALSMLLATAFVAMPAGADTKIGFVNTERLLREAPLSVAAQKKLEREFAGRDQEL 61

>[gi|53719759|ref|YP_108745.1|](#)  putative outer membrane protein [Burkholderia ps
K96243]
[gi|53723730|ref|YP_103186.1|](#)  outer membrane protein, OmpH/HlpA family [Burkhold
ATCC 23344]
[gi|52427153|gb|AAU47746.1|](#)  outer membrane protein, OmpH/HlpA family [Burkholder
ATCC 23344]
[gi|52210173|emb|CAH36152.1|](#)  putative outer membrane protein [Burkholderia pseud
K96243]
Length = 177

Score = 32.7 bits (73), Expect = 2.8
Identities = 22/51 (43%), Positives = 26/51 (50%), Gaps = 1/51 (1%)

Query: 11 LACLLVANSAFSADFP-IGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
LA L A +A + D I NS I ES AKAQ KL++EF L
Sbjct: 16 LAAALGATAARAQDVARIAAVNSDRILRESAPAKAAQTKLEAEFAKRDKDL 66

>[gi|9949807|gb|AAG07035.1|](#)  probable outer membrane protein precursor [Pseudom
PAO1]
[gi|11351575|pir||G83190](#) probable outer membrane protein precursor PA3647 [importe
Pseudomonas aeruginosa (strain PAO1)]
[gi|20139187|sp|Q9HXY5|OMPH_PSEAE](#) OmpH-like protein precursor
[gi|15598843|ref|NP_252337.1|](#)  probable outer membrane protein precursor [Pseudom
PAO1]
Length = 168

Score = 32.7 bits (73), Expect = 2.8
Identities = 21/60 (35%), Positives = 32/60 (53%), Gaps = 1/60 (1%)

Query: 1 MKVKTLMAILACLLVANSAFSADFP-IGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
M+ T + I A ++ A SAF A+ I V N Q +ES+AAK + +FG + +L
Sbjct: 1 MRKFTQFVLITAAIMAAPSAF-AEMKIAVLNYQMALLESDAKQYAVDAEKKFGPQLNKL 59

>[gi|49081394|gb|AAT50125.1|](#) PA3647 [synthetic construct]
Length = 169

Score = 32.7 bits (73), Expect = 2.8
Identities = 21/60 (35%), Positives = 32/60 (53%), Gaps = 1/60 (1%)

Query: 1 MKVKTLMAILACLLVANSAFSAFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
M+ T + I A ++ A SAF A+ I V N Q +ES+AAK + +FG + +L
Sbjct: 1 MRKFTQFVLITAAIMAAPSAF-AEMKIAVLNYQMALLESDAAKQYAVDAEKKFGPQLNKL 59

>[gi|51597309|ref|YP_071500.1|](#) **G** cationic 19 kDa outer membrane protein precursor
pseudotuberculosis IP 32953]
[gi|51590591|emb|CAH22232.1|](#) **G** cationic 19 kDa outer membrane protein precursor [Y
pseudotuberculosis IP 32953]
Length = 182

Score = 32.0 bits (71), Expect = 4.8
Identities = 19/57 (33%), Positives = 29/57 (50%)

Query: 4 KTLMAILACLLVANSAFSAFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
K L A L L A+++ A I + N SI + A +A K+L++EF T+L
Sbjct: 20 KWLCAASLGLALAASASVQAADKIAIVNVSSIFQQLPAREAVAKQLENEFKGRATEL 76

>[gi|45442565|ref|NP_994104.1|](#) **G** cationic 19 kDa outer membrane protein precursor
biovar Medievalis str. 91001]
[gi|22127002|ref|NP_670425.1|](#) **G** automembrane protein H [Yersinia pestis KIM]
[gi|45437430|gb|AAS62981.1|](#) **G** cationic 19 kDa outer membrane protein precursor [Ye
biovar Medievalis str. 91001]
[gi|21960048|gb|AAM86676.1|](#) **G** automembrane protein H [Yersinia pestis KIM]
Length = 196

Score = 32.0 bits (71), Expect = 4.8
Identities = 19/57 (33%), Positives = 29/57 (50%)

Query: 4 KTLMAILACLLVANSAFSAFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
K L A L L A+++ A I + N SI + A +A K+L++EF T+L
Sbjct: 34 KWLCAASLGLALAASASVQAADKIAIVNVSSIFQQLPAREAVAKQLENEFKGRATEL 90

>[gi|16121353|ref|NP_404666.1|](#) **G** cationic 19 kDa outer membrane protein precursor
CO92]
[gi|15979120|emb|CAC89895.1|](#) **G** cationic 19 kDa outer membrane protein precursor [Y
CO92]
[gi|20138917|sp|P58607|OMPH YERPE](#) Cationic 19 kDa outer membrane protein precursor
[gi|55977788|sp|P31520|OMPH YERPS](#) Cationic 19 kDa outer membrane protein precursor
[gi|25294338|pir|AD0129](#) cationic 19 kDa outer membrane protein precursor ompH [im
- Yersinia pestis (strain CO92)
Length = 165

Score = 32.0 bits (71), Expect = 4.8
Identities = 19/57 (33%), Positives = 29/57 (50%)

Query: 4 KTLMAILACLLVANSAFSAFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
K L A L L A+++ A I + N SI + A +A K+L++EF T+L
Sbjct: 3 KWLCAASLGLALAASASVQAADKIAIVNVSSIFQQLPAREAVAKQLENEFKGRATEL 59

>[gi|51246715|ref|YP_066599.1|](#) **G** hypothetical protein DP2863 [Desulfotalea psych
[gi|50877752|emb|CAG37592.1|](#) **G** unknown protein [Desulfotalea psychrophila LSv54]
Length = 185

Score = 32.0 bits (71), Expect = 4.8
Identities = 17/50 (34%), Positives = 31/50 (62%), Gaps = 1/50 (2%)

Query: 4 KTLMAILA-CLLVANSAFSAFPIGVFNSQSIAMESEAAKAAQKKLQSE 52
K+L + +L+ C L +SA++A IGV + Q I E +A K A +++++
Sbjct: 16 KSLFVVVLSVCALFVSSAYAAVTKIGVMDVQKIITECKAGKTASARVEAK 65

>[gi|46164357|ref|ZP_00205054.1|](#) COG2825: Outer membrane protein [Pseudomonas aeruginosa] UCBPP-PA14]
Length = 173

Score = 32.0 bits (71), Expect = 4.8
Identities = 20/56 (35%), Positives = 30/56 (53%), Gaps = 1/56 (1%)

Query: 5 TLMAILACLLVANSAFSAFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
T + I A ++ A SAF A+ I V N Q +ES+AAK + +FG + +L
Sbjct: 10 TQFVLITAAIMAAPSAF-AEMKIAVLNYQMALLESDAAKQYAVDAEKKFGPQLNKL 64

>[gi|30249671|ref|NP_841741.1|](#) putative transmembrane protein [Nitrosomonas europaea]
[gi|30180708|emb|CAD85620.1|](#) putative transmembrane protein [Nitrosomonas europaea]
Length = 187

Score = 31.6 bits (70), Expect = 6.3
Identities = 19/51 (37%), Positives = 29/51 (56%), Gaps = 2/51 (3%)

Query: 3 VKTLMAILACLLVANSAFSAFPIGVFNSQSIAMESEAAKAAQKKLQSEF 53
VK + ++ L V +SA + IGV N++ + ES A AQKK++ EF
Sbjct: 17 VKAFVVVTMMFVLPVHSSA--GEIKIGVVNTEKVLRESMPAIEAQKKIEREF 65

>[gi|34103516|gb|AAQ59878.1|](#) outer membrane protein [Chromobacterium violaceum]
[gi|34497660|ref|NP_901875.1|](#) outer membrane protein [Chromobacterium violaceum]
Length = 161

Score = 31.6 bits (70), Expect = 6.3
Identities = 17/58 (29%), Positives = 28/58 (48%)

Query: 3 VKTLMAILACLLVANSAFSAFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
+K L + + A +ADF +G N + I E+ + A KKL EF + + +L
Sbjct: 1 MKALKWWLAVLSVAALPVHAADFKLGFVNIERIYREAGVSVAIYKKLDKEFSSRREEL 58

>[gi|46319050|ref|ZP_00219470.1|](#) COG2825: Outer membrane protein [Burkholderia cepacia]
Length = 166

Score = 31.6 bits (70), Expect = 6.3
Identities = 21/51 (41%), Positives = 26/51 (50%), Gaps = 1/51 (1%)

Query: 11 LACLLVANSAFSAFPIGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
+A L A +A + D I NS I ES AKAAQ KL++EF L
Sbjct: 7 IALALGAATAHAQDVARIAAVNSDRILRESAPAKAAQTKLEAEFAKRDKDL 57

>[gi|53761352|ref|ZP_00166830.2|](#) COG2825: Outer membrane protein [Ralstonia eutropha]
Length = 148

Score = 31.2 bits (69), Expect = 8.2
Identities = 15/34 (44%), Positives = 20/34 (58%)

Query: 27 IGVFNSQSIAMESEAAKAAQKKLQSEFGNEKTQL 60
I NS+ I +S+ AKAAQ KL+ EF +L

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
Posted date: Mar 3, 2005 10:03 AM
Number of letters in database: 793,074,205
Number of sequences in database: 2,340,000

Lambda	K	H
0.315	0.123	0.314

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 14,682,859
Number of Sequences: 2340000
Number of extensions: 305533
Number of successful extensions: 1709
Number of sequences better than 10:0: 7
Number of HSP's better than 10.0 without gapping: 4
Number of HSP's successfully gapped in prelim test: 3
Number of HSP's that attempted gapping in prelim test: 1705
Number of HSP's gapped (non-prelim): 7
length of query: 60
length of database: 793,074,205
effective HSP length: 32
effective length of query: 28
effective length of database: 718,194,205
effective search space: 20109437740
effective search space used: 20109437740
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.6 bits)
S2: 69 (31.2 bits)